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# UniProtKB/Swiss-Prot entry

## P47154

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### Entry information

Entry name	STE24_YEAST
Primary accession number	P47154
Secondary accession numbers	None
Integrated into Swiss-Prot on	February 1, 1996
Sequence was last modified on	February 1, 1996 (Sequence version 1)
Annotations were last modified on	September 2, 2008 (Entry version 73)
Name and origin of the protein	
Protein name	CAAX prenyl protease 1
Synonyms	EC 3.4.24.84 Prenyl protein-specific endoprotease 1 PPSEP 1 A-factor-converting enzyme
Gene name	Name: STE24 Synonyms: AFC1 OrderedLocusNames: YJR117W ORFNames: J2032
From	Saccharomyces cerevisiae (Baker's yeast) [TaxID: 4932]
Taxonomy	Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Protein existence	1: Evidence at protein level;

### References

- [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.  
DOI=10.1083/jcb.136.2.271; PubMed=9015299 [NCBI, ExPASy, EBI, Israel, Japan]  
Fujimura-Kamada K., Nouvet F.J., Michaelis S.;  
"A novel membrane-associated metalloprotease, Ste24p, is required for the first step of NH2-terminal processing of the yeast a-factor precursor."  
J. Cell Biol. 136:271-285(1997).

- [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
STRAIN=ATCC 96604 / S288c / FY1679;  
PubMed=8641269 [NCBI, ExPASy, EBI, Israel, Japan]  
Galibert F., Alexandraki D., Baur A., Boles E., Chalwatzis N., Chuat J.-C., Coster F., Cziepluch C., de Haan M., Domdey H., Durand P., Entian K.-D., Gattius M., Goffeau A., Grivell L.A., Hennemann A., Herbert C.J., Heumann K., Hilger F., , Karpfinger-Hartl L.;  
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EMBO J. 15:2031-2049(1996).
- [3] FUNCTION.  
DOI=10.1126/science.275.5307.1796; PubMed=9065405 [NCBI, ExPASy, EBI, Israel, Japan]  
Boyartchuk V.L., Ashby M.N., Rine J.;  
"Modulation of Ras and a-factor function by carboxyl-terminal proteolysis.";  
Science 275:1796-1800(1997).
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DOI=10.1083/jcb.142.3.635; PubMed=9700155 [NCBI, ExPASy, EBI, Israel, Japan]  
Tam A., Nouvet F.J., Fujimura-Kamada K., Slunt H., Sisodia S.S., Michaelis S.;  
"Dual roles for Ste24p in yeast a-factor maturation: NH2-terminal proteolysis and COOH-terminal CAA processing.";  
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PubMed=9725832 [NCBI, ExPASy, EBI, Israel, Japan]  
Boyartchuk V.L., Rine J.;  
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Genetics 150:95-101(1998).
- [6] FUNCTION.  
DOI=10.1074/jbc.275.9.6227; PubMed=10692417 [NCBI, ExPASy, EBI, Israel, Japan]  
Schmidt W.K., Tam A., Michaelis S.;  
"Reconstitution of the Ste24p-dependent N-terminal proteolytic step in yeast a-Factor biogenesis.";  
J. Biol. Chem. 275:6227-6233(2000).
- [7] CHARACTERIZATION.  
DOI=10.1128/MCB.20.12.4381-4392.2000; PubMed=10825201 [NCBI, ExPASy, EBI, Israel, Japan]  
Trueblood C.E., Boyartchuk V.L., Picologlou E.A., Rozema D., Poulter C.D., Rine J.;  
"The CaaX proteases, Afc1p and Rce1p, have overlapping but distinct substrate specificities.";  
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- [8] SUBCELLULAR LOCATION.  
DOI=10.1073/pnas.95.19.11175; PubMed=9736709 [NCBI, ExPASy, EBI, Israel, Japan]  
Schmidt W.K., Tam A., Fujimura-Kamada K., Michaelis S.;  
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Proc. Natl. Acad. Sci. U.S.A. 95:11175-11180(1998).
- [9] LEVEL OF PROTEIN EXPRESSION [LARGE SCALE ANALYSIS].  
DOI=10.1038/nature02046; PubMed=14562106 [NCBI, ExPASy, EBI, Israel, Japan]  
Ghaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A., Dephoure N., O'Shea E.K., Weissman J.S.;  
"Global analysis of protein expression in yeast.";  
Nature 425:737-741(2003).
- [10] TOPOLOGY [LARGE SCALE ANALYSIS].  
DOI=10.1073/pnas.0604075103; PubMed=16847258 [NCBI, ExPASy, EBI, Israel, Japan]  
Kim H., Melen K., Oesterberg M., von Heijne G.;  
"A global topology map of the *Saccharomyces cerevisiae* membrane proteome.";  
Proc. Natl. Acad. Sci. U.S.A. 103:11142-11147(2006).

Comments

- **FUNCTION:** Proteolytically removes the C-terminal three residues of farnesylated A-factor mating pheromone. Also acts to cleave the N-terminal extension of the pheromone. Does not act on Ras.
- **CATALYTIC ACTIVITY:** The peptide bond hydrolyzed can be designated -C[-A-A-X in which C is an S-isoprenylated cysteine residue, A is usually aliphatic and X is the C-terminal residue of the substrate protein, and may be any of several amino acids.
- **COFACTOR:** Binds 1 zinc ion per subunit (*By similarity*).
- **INTERACTION:**  
P10592:SSA2; NbExp=1; IntAct=EBI-18298, EBI-8603;
- **SUBCELLULAR LOCATION:** Endoplasmic reticulum membrane; Multi-pass membrane protein.
- **MISCELLANEOUS:** Present with 19600 molecules/cell in log phase SD medium.
- **SIMILARITY:** Belongs to the peptidase M48A family [view classification].

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#### Cross-references

##### Sequence databases

EMBL U77137; AAB38271.1; -; Genomic\_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]  
Z49617; CAA89647.1; -; Genomic\_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]  
PIR S57140; S57140.  
RefSeq NP\_012651.1; -.

##### 3D structure databases

ModBase P47154.

##### Protein-protein interaction databases

DIP DIP:1390N; -.  
IntAct P47154; -.

##### Protein family/group databases

MEROPS M48.001; -.

##### Organism-specific databases

CYGD YJR117w; -.  
SGD S000003878; STE24.  
Yeast-GFP YJR117W.

##### Gene expression databases

GermOnline YJR117W; *Saccharomyces cerevisiae*.

##### Ontologies

GO GO:0030176; Cellular component: integral to endoplasmic reticulum membrane (*inferred from direct assay from SGD*).  
GO:0005741; Cellular component: mitochondrial outer membrane (*inferred from direct assay from SGD*).  
GO:0008487; Molecular function: prenyl-dependent CAAX protease activity (*inferred from direct assay from SGD*).  
GO:0005515; Molecular function: protein binding (*inferred from physical interaction from IntAct*).  
GO:0007323; Biological process: peptide pheromone maturation (*inferred from direct assay from SGD*).  
QuickGo  
view.

##### Family and domain databases

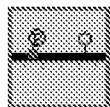
InterPro IPR006025; Pept\_M\_Zn\_BS.  
IPR001915; Peptidase\_M48.  
Graphical view of domain structure.

**Pfam** PF01435; Peptidase\_M48; 1.  
 Pfam graphical view of domain structure.  
**PROSITE** PS00142; ZINC\_PROTEASE; 1.  
**BLOCKS** P47154.  
**Proteomic databases**  
**PeptideAtlas** P47154; -.  
**Genome annotation databases**  
**Ensembl** YJR117W; *Saccharomyces cerevisiae*. [Contig view]  
**GeneID** 853581; -.  
**GenomeReviews** Y13136\_GR; YJR117W.  
**KEGG** sce:YJR117W; -.  
**NMPDR** fig|4932.3.peg.3626; -.  
**Phylogenomic databases**  
**HOGENOM** P47154; -.  
**Other**  
**LinkHub** P47154; -.  
**ProtoNet** P47154.  
**UniRef** View cluster of proteins with at least 50% / 90% / 100% identity.

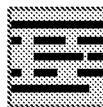
### Keywords

Complete proteome; Endoplasmic reticulum; Hydrolase; Membrane; Metal-binding; Metalloprotease; Pheromone response; Protease; Transmembrane; Zinc.

### Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FTId
CHAIN	1	453	453	CAAX prenyl protease 1.	PRO_0000138846
TOPO_DOM	1	12	12	Lumenal (Potential).	
TRANSMEM	13	33	21	Potential.	
TOPO_DOM	34	89	56	Cytoplasmic (Potential).	
TRANSMEM	90	110	21	Potential.	
TOPO_DOM	111	121	11	Lumenal (Potential).	
TRANSMEM	122	142	21	Potential.	
TOPO_DOM	143	167	25	Cytoplasmic (Potential).	
TRANSMEM	168	188	21	Potential.	
TOPO_DOM	189	197	9	Lumenal (Potential).	
TRANSMEM	198	218	21	Potential.	
TOPO_DOM	219	306	88	Cytoplasmic (Potential).	
TRANSMEM	307	327	21	Potential.	
TOPO_DOM	328	357	30	Lumenal (Potential).	
TRANSMEM	358	378	21	Potential.	
TOPO_DOM	379	453	75	Cytoplasmic (Potential).	
ACT_SITE	298	298		By similarity.	
ACT_SITE	394	394		Proton donor (By similarity).	
METAL	297	297		Zinc; catalytic (By similarity).	
METAL	301	301		Zinc; catalytic (By similarity).	
METAL	390	390		Zinc; catalytic (By similarity).	

### Sequence information

Length: 453 AA [This is the length of the unprocessed precursor]

Molecular weight: 52324 Da [This is the MW of the unprocessed precursor]

CRC64: 331CC9AE2D7C99DA [This is a checksum on the sequence]

```

      10           20           30           40           50           60
MFDLKTILDH PNIPWKLIIS GFSIAQFSFE SYLTYRQYQK LSETKLPPVL EDEIDDETFF

      70           80           90          100          110          120
KSRNYSRAKA KFSIFGDVYN LAQKLVIKY DLFPKIWHMA VSLLNAVLPV RFHMOVSTVAQ

     130          140          150          160          170          180
SLCFLGILLSS LSTLVLDPLS YYSHFVLEEK FGFNKLTVQL WITDMIKSLT LAYAIGGPIL

     190          200          210          220          230          240
YLFLKIFDKF PTDFLWYIMV FLFVVQILAM TIIPVFIMPM FNKFTPLEDG ELKKSIESLA

     250          260          270          280          290          300
DRVGFPLDKI FVIDGSKRSS HSNAYFTGLP FTSKRIVLFD TLVNSNSTDE ITAVLAHEIG

     310          320          330          340          350          360
HWQKNHIVNM VIFSQLHTFL IFSLFTSIYR NTSFYNTFGF FLEKSTGSFV DPVITKEFPI

     370          380          390          400          410          420
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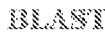
     430          440          450
MNVDPYSSY HYSHPTLAER LTALDYVSEK KKN
  
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P47154 in  
FASTA format

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 BLAST submission on  
ExPASy/SIB  
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,  
Compute pI/Mw, PeptideMass, PeptideCutter,  
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-  
MODEL



NPSA Sequence analysis  
tools



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